



10077137 Sequence Listing
SEQUENCE LISTING

<110> MACKAY, FABIENNE
BROWNING, JEFFREY
AMBROSE, CHRISTINE
TSCHOPP, JURG
SCHNEIDER, PASCAL
THOMPSON, JEFFREY

<120> BAFF RECEPTOR (BCMA), AN IMMUNOREGULATORY AGENT

<130> 08201.0027

<140> 10/077,137
<141> 2002-02-15

<150> PCT/US00/22507
<151> 2000-08-16

<150> 60/149,378
<151> 1999-08-17

<150> 60/181,684
<151> 2000-02-11

<150> 60/183,536
<151> 2000-02-18

<160> 9

<170> PatentIn Ver. 3.3

<210> 1
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<213> Homo sapiens

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Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30

Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
50 55 60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65 70 75 80

Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
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130 135 140

Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 145 150 155 160

Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
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Ile Glu Lys Ser Ile Ser Ala Arg
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acattgacct	ggaaaagagc	aggactggtg	atgaaattat	tctccgagag	gcctcgagta	360
cacgtggaa	gaatgcacct	gtgaagactg	catcaagagc	aaaccgaagg	tcgactctga	420
ccatgtctt	ccactcccag	ctatggagga	aggcgcaacc	attctgtcac	cacgaaaacg	480
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<212> PRT

<213> Homo sapiens

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20	25	30				

Asp Ser Leu Asp Val Thr Met Leu Gln Met Ala Gly Gln Cys Ser Gln						
35	40	45				

Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu						
50	55	60				

Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Leu His Ala Cys Ile						
65	70	75	80			

Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln						
85	90	95				

Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Gln Arg Tyr						
100	105	110				

Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Val Asp Lys Thr His						
115	120	125				

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val						
130	135	140				

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
165 170 175

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
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Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val
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<213> Homo sapiens

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<213> Homo sapiens

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20 25 30

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
35 40 45

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
50 55 60

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
65 70 75 80

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
85 90 95

Gly Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
100 105 110

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<213> Homo sapiens

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cagccggaga acaactaca gaccacgcct cccgtgttgg actccgacgg ctcccttc 240
ctctacagca agtcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 300
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<210> 7
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<213> Homo sapiens

<400> 7
Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser
1 5 10 15
Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr
20 25 30
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
35 40 45
Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
50 55 60
Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
65 70 75 80
Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
85 90 95
Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
100 105 110
Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
115 120 125
Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
130 135 140
Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
145 150 155 160
Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
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Ile Glu Lys Ser Ile Ser Ala Arg
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<212> DNA

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agctgctctt gctgcatttg ctcttggatt cttgttagaga tattacttgt cttccaggc 180
tgttcttctt gtagctccct tttttcttt ttgtgatcat gttgcagatg gctgggcagt 240
gctcccaaaa tgaatatttt gacagtttg tgcatttttgcataccttgt caacttcgtat 300
gttcttctaa tactccctctt ctaacatgtc agcgttatttg taatgcaagt gtgaccaatt 360
cagtgaaagg aacgaatgcg atttcttggc cctgtttggg actgagctta ataatttctt 420
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					20			25			30				
Arg	Lys	Glu	Ser	Pro	Ser	Val	Arg	Ser	Ser	Lys	Asp	Gly	Lys	Leu	Leu
					35		40			45					
Ala	Ala	Thr	Leu	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Cys	Leu	Thr	Val	Val
	50				55					60					
Ser	Phe	Tyr	Gln	Val	Ala	Ala	Leu	Gln	Gly	Asp	Leu	Ala	Ser	Leu	Arg
	65			70				75			80				
Ala	Glu	Leu	Gln	Gly	His	His	Ala	Glu	Lys	Leu	Pro	Ala	Gly	Ala	Gly
					85			90			95				
Ala	Pro	Lys	Ala	Gly	Leu	Glu	Glu	Ala	Pro	Ala	Val	Thr	Ala	Gly	Leu
	100				105						110				
Lys	Ile	Phe	Glu	Pro	Pro	Ala	Pro	Gly	Glu	Gly	Asn	Ser	Ser	Gln	Asn
	115				120						125				
Ser	Arg	Asn	Lys	Arg	Ala	Val	Gln	Gly	Pro	Glu	Glu	Thr	Val	Thr	Gln
	130			135						140					
Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys
	145				150				155				160		
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					165			170			175				
Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr
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Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
195 200 205

Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
210 215 220

Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
225 230 235 240

Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
245 250 255

Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
260 265 270

Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
275 280 285